



SEQUENCE LISTING

<110> Wolfrum, Science A
Letterio, John J

<120> FUNCTIONALIZED TGF-BETA FUSION PROTEINS

<130> 4239-61302

<140> US 10/017,372

<141> 2001-10-19

<150> US 60/242,292

<151> 2000-10-20

<160> 39

<170> PatentIn version 3.1

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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ggagagatct ggtaccgaga tggcgcct

28

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ataagaattg cggccgcttt aatcgatccc aagtgggctt gg

42

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45

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45

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<400> 7

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 8
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<222> (1)..(1197)
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<222> (278)..(279)

<223> Maturation cleavage site

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1 5 10 15	
tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc	96
Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr	
20 25 30	
tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc	144
Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala	
35 40 45	
att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc	192
Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser	
50 55 60	
cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt	240
Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu	
65 70 75 80	
tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag	288
Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu	
85 90 95	
ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta	336
Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu	
100 105 110	
atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc	384
Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro	
115 120 125	
cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg	432
His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val	
130 135 140	
ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc	480
Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu	
145 150 155 160	
aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat	528
Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn	
165 170 175	
gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca	576
Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser	
180 185 190	
ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg	624
Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu	
195 200 205	
acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc	672
Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser	
210 215 220	
tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat	720

Ser	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn	Gly	Phe	Asn		
225					230					235					240		
tct	ggc	cgc	cgg	ggt	gac	ctg	gcc	acc	att	cac	ggc	atg	aac	cgg	ccc		768
Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met	Asn	Arg	Pro		
				245					250					255			
ttc	ctg	ctc	ctc	atg	gcc	acc	ccg	ctg	gag	agg	gcc	cag	cac	ctg	cac		816
Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	His	Leu	His		
				260				265					270				
agc	tcc	cgg	cac	cgc	cga	gac	tac	aag	gat	gac	gac	gac	aag	gcc	ctg		864
Ser	Ser	Arg	His	Arg	Arg	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ala	Leu		
		275					280					285					
gat	acc	aac	tac	tgc	ttc	agc	tcc	acg	gag	aag	aac	tgc	tgc	gtg	cgg		912
Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	Thr	Glu	Lys	Asn	Cys	Cys	Val	Arg		
	290					295					300						
cag	ctc	tac	att	gac	ttc	cgg	aag	gac	ctg	ggc	tgg	aag	tgg	att	cat		960
Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp	Lys	Trp	Ile	His		
305					310					315					320		
gaa	ccc	aag	ggc	tac	cat	gcc	aat	ttc	tgc	ctg	ggg	ccc	tgt	ccc	tac		1008
Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Leu	Gly	Pro	Cys	Pro	Tyr		
				325					330					335			
atc	tgg	agc	cta	gac	act	cag	tac	agc	aag	gtc	ctg	gct	ctg	tac	aac		1056
Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	Ser	Lys	Val	Leu	Ala	Leu	Tyr	Asn		
			340					345						350			
cag	cac	aac	ccg	ggc	gcg	tcg	gcg	gcg	ccg	tgc	tgc	gtg	ccg	cag	gcg		1104
Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	Ala	Pro	Cys	Cys	Val	Pro	Gln	Ala		
		355					360					365					
ctg	gag	cca	ctg	ccc	atc	gtg	tac	tac	gtg	ggc	cgc	aag	ccc	aag	gtg		1152
Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	Tyr	Val	Gly	Arg	Lys	Pro	Lys	Val		
	370					375					380						
gag	cag	ctg	tcc	aac	atg	atc	gtg	cgt	tcc	tgc	aag	tgc	agc	tga			1197
Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Arg	Ser	Cys	Lys	Cys	Ser				
385					390					395							

<210> 9
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<220>
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<220>
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 <222> (278)..(279)
 <223> Maturation cleavage site

<400> 9

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20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
 275 280 285

Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
 290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
 305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
 325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
 340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
 355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
 370 375 380

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 385 390 395

<210> 10
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 <212> DNA
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<220>
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 attcatgaac ccaagggctc catgccaaatt tctgcctggg gccctgtccc tacatctgga 180
 gcctagacac tcagtacagc aaggctcctg ctctgtacaa ccagcacaac ccgggcgcggt 240
 cggcgggcgcc gtgctgctgt cgcagggcgc tggagccact gccatcgtg tactacgtgg 300
 gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttctctgc aagtgcagct 360
 ga 362

<210> 11
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<212> PRT
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<220>
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<222> (1)..(8)
<223> FLAG tag

<400> 11

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Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
20 25 30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
115 120

<210> 12
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<212> DNA
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<222> (1)..(1197)
<223>

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 <222> (278)..(279)
 <223> Maturation cleavage site

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 1 5 10 15
 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc 96
 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30
 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45
 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192
 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60
 cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt 240
 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80
 tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag 288
 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95
 ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta 336
 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110
 atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc 384
 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125
 cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg 432
 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140
 ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc 480
 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160
 aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat 528
 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175
 gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca 576
 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190
 ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg 624
 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205
 acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc 672

Thr	Arg	Arg	Glu	Ala	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala	His	Ser	Ser	
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tct	gac	agc	aaa	gat	aac	aca	ctc	cac	gtg	gaa	att	aac	ggg	ttc	aat	720
Ser	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn	Gly	Phe	Asn	
225					230					235					240	
tct	ggc	cgc	cgg	ggt	gac	ctg	gcc	acc	att	cac	ggc	atg	aac	cgg	ccc	768
Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met	Asn	Arg	Pro	
				245					250					255		
ttc	ctg	ctc	ctc	atg	gcc	acc	ccg	ctg	gag	agg	gcc	cag	cac	ctg	cac	816
Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	His	Leu	His	
			260					265					270			
agc	tcc	cgg	cac	cgc	cga	gcc	ctg	gat	acc	aac	tac	tgc	ttc	agc	tcc	864
Ser	Ser	Arg	His	Arg	Arg	Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	
		275					280					285				
acg	gac	tac	aag	gat	gac	gac	gac	aag	gag	aag	aac	tgc	tgc	gtg	cgg	912
Thr	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Glu	Lys	Asn	Cys	Cys	Val	Arg	
	290				295						300					
cag	ctc	tac	att	gac	ttc	cgg	aag	gac	ctg	ggc	tgg	aag	tgg	att	cat	960
Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp	Lys	Trp	Ile	His	
305				310						315					320	
gaa	ccc	aag	ggc	tac	cat	gcc	aat	ttc	tgc	ctg	ggg	ccc	tgt	ccc	tac	1008
Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Leu	Gly	Pro	Cys	Pro	Tyr	
			325						330					335		
atc	tgg	agc	cta	gac	act	cag	tac	agc	aag	gtc	ctg	gct	ctg	tac	aac	1056
Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	Ser	Lys	Val	Leu	Ala	Leu	Tyr	Asn	
			340					345					350			
cag	cac	aac	ccg	ggc	gcg	tcg	gcg	gcg	ccg	tgc	tgc	gtg	ccg	cag	gcg	1104
Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	Ala	Pro	Cys	Cys	Val	Pro	Gln	Ala	
		355					360					365				
ctg	gag	cca	ctg	ccc	atc	gtg	tac	tac	gtg	ggc	cgc	aag	ccc	aag	gtg	1152
Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	Tyr	Val	Gly	Arg	Lys	Pro	Lys	Val	
	370				375					380						
gag	cag	ctg	tcc	aac	atg	atc	gtg	cgt	tcc	tgc	aag	tgc	agc	tga		1197
Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Arg	Ser	Cys	Lys	Cys	Ser			
385				390						395						

<210> 13
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion oligonucleotide

<220>
 <221> misc_feature
 <222> (278)..(279)
 <223> Maturation cleavage site

<400> 13

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Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
 275 280 285

Thr Asp Tyr Lys Asp Asp Asp Asp Lys Glu Lys Asn Cys Cys Val Arg
 290 295 300

Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
 305 310 315 320

Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
 325 330 335

Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
 340 345 350

Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
 355 360 365

Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
 370 375 380

Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 385 390 395

<210> 14
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 <212> DNA
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<220>
 <223> Fusion oligonucleotide

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 attcatgaac ccaagggtcta ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg 180
 agcctagaca ctcagtacac aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt 240
 cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcgtg tactacgtgg 300
 gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttcctgc aagtgcagct 360

<210> 15
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion oligopeptide

<220>
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 <222> (12)..(19)
 <223> FLAG tag

<400> 15

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Asp Tyr Lys Asp Asp
 1 5 10 15

Asp Asp Lys Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
 20 25 30

Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
 35 40 45

Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
 50 55 60

Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
 65 70 75 80

Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
 85 90 95

Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
 100 105 110

Ile Val Arg Ser Cys Lys Cys Ser
 115 120

<210> 16
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 <222> (1560)..(1612)
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<220>
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 <222> (1182)..(1196)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (1197)..(1220)
 <223> Encodes FLAG epitope tag

<220>
 <221> misc_feature
 <222> (1182)..(1159)
 <223> Encodes ature fusion protein

<220>
 <221> misc_feature
 <222> (1182)..(1159)
 <223> Encodes mature fusion protein

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 agagcgctca tctcgatatt taccctggtg gtatactgag acaccttggt gtcagagcct 180
 caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct 240
 ttccttgga gacccaccc cacaagccct gcaggggcgg ggctccgca tccaccttt 300
 gccgagggtt cccgctctcc gaagtgccgt ggggcgcgc ctcccc atg ccg ccc 356
 Met Pro Pro
 1
 tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta 404
 Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro Trp Leu Leu
 5 10 15
 gtg ctg acg ccc ggg agg cca gcc gcg gga ctc tcc acc tgc aag acc 452

Val	Leu	Thr	Pro	Gly	Arg	Pro	Ala	Ala	Gly	Leu	Ser	Thr	Cys	Lys	Thr		
20					25					30					35		
atc	gac	atg	gag	ctg	gtg	aaa	cgg	aag	cgc	atc	gaa	gcc	atc	cgt	ggc		500
Ile	Asp	Met	Glu	Leu	Val	Lys	Arg	Lys	Arg	Ile	Glu	Ala	Ile	Arg	Gly		
				40					45					50			
cag	atc	ctg	tcc	aaa	cta	agg	ctc	gcc	agt	ccc	cca	agc	cag	ggg	gag		548
Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Ala	Ser	Pro	Pro	Ser	Gln	Gly	Glu		
			55					60					65				
gta	ccg	ccc	ggc	ccg	ctg	ccc	gag	gcg	gtg	ctc	gct	ttg	tac	aac	agc		596
Val	Pro	Pro	Gly	Pro	Leu	Pro	Glu	Ala	Val	Leu	Ala	Leu	Tyr	Asn	Ser		
		70					75					80					
acc	cgc	gac	cgg	gtg	gca	ggc	gag	agc	gcc	gac	cca	gag	ccg	gag	ccc		644
Thr	Arg	Asp	Arg	Val	Ala	Gly	Glu	Ser	Ala	Asp	Pro	Glu	Pro	Glu	Pro		
	85					90					95						
gaa	gcg	gac	tac	tat	gct	aaa	gag	gtc	acc	cgc	gtg	cta	atg	gtg	gac		692
Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr	Arg	Val	Leu	Met	Val	Asp		
100					105					110					115		
cgc	aac	aac	gcc	atc	tat	gag	aaa	acc	aaa	gac	atc	tca	cac	agt	ata		740
Arg	Asn	Asn	Ala	Ile	Tyr	Glu	Lys	Thr	Lys	Asp	Ile	Ser	His	Ser	Ile		
				120					125					130			
tat	atg	ttc	ttc	aat	acg	tca	gac	att	cgg	gaa	gca	gtg	ccc	gaa	ccc		788
Tyr	Met	Phe	Phe	Asn	Thr	Ser	Asp	Ile	Arg	Glu	Ala	Val	Pro	Glu	Pro		
				135				140					145				
cca	ttg	ctg	tcc	cgt	gca	gag	ctg	cgc	ttg	cag	aga	tta	aaa	tca	agt		836
Pro	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu	Gln	Arg	Leu	Lys	Ser	Ser		
		150					155					160					
gtg	gag	caa	cat	gtg	gaa	ctc	tac	cag	aaa	tat	agc	aac	aat	tcc	tgg		884
Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys	Tyr	Ser	Asn	Asn	Ser	Trp		
	165					170					175						
cgt	tac	ctt	ggt	aac	cgg	ctg	ctg	acc	ccc	act	gat	acg	cct	gag	tgg		932
Arg	Tyr	Leu	Gly	Asn	Arg	Leu	Leu	Thr	Pro	Thr	Asp	Thr	Pro	Glu	Trp		
180					185					190					195		
ctg	tct	ttt	gac	gtc	act	gga	gtt	gta	cgg	cag	tgg	ctg	aac	caa	gga		980
Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg	Gln	Trp	Leu	Asn	Gln	Gly		
				200					205					210			
gac	gga	ata	cag	ggc	ttt	cga	ttc	agc	gct	cac	tgc	tct	tgt	gac	agc		1028
Asp	Gly	Ile	Gln	Gly	Phe	Arg	Phe	Ser	Ala	His	Cys	Ser	Cys	Asp	Ser		
			215					220					225				
aaa	gat	aac	aaa	ctc	cac	gtg	gaa	atc	aac	ggg	atc	agc	ccc	aaa	cgt		1076
Lys	Asp	Asn	Lys	Leu	His	Val	Glu	Ile	Asn	Gly	Ile	Ser	Pro	Lys	Arg		
		230					235					240					
cgg	ggc	gac	ctg	ggc	acc	atc	cat	gac	atg	aac	cgg	ccc	ttc	ctg	ctc		1124
Arg	Gly	Asp	Leu	Gly	Thr	Ile	His	Asp	Met	Asn	Arg	Pro	Phe	Leu	Leu		
	245					250					255						
ctc	atg	gcc	acc	ccc	ctg	gaa	agg	gcc	cag	cac	ctg	cac	agc	tca	cgg		1172
Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	His	Leu	His	Ser	Ser	Arg		

260	265	270	275	
cac cgg aga gcc ctg gat acc aac gac tac aag gat gac gac gac aag				1220
His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp Asp Asp Lys				
	280	285	290	
gcc ctg gat acc aac tat tgc ttc agc tcc aca gag aag aac tgc tgt				1268
Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys				
	295	300	305	
gtg cgg cag ctg tac att gac ttt agg aag gac ctg ggt tgg aag tgg				1316
Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp				
	310	315	320	
atc cac gag ccc aag ggc tac cat gcc aac ttc tgt ctg gga ccc tgc				1364
Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys				
	325	330	335	
ccc tat att tgg agc ctg gac aca cag tac agc aag gtc ctt gcc ctc				1412
Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu				
	340	345	350	355
tac aac caa cac aac ccg ggc gct tgc gcg tca ccg tgc tgc gtg ccg				1460
Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys Cys Val Pro				
	360	365	370	
cag gct ttg gag cca ctg ccc atc gtc tac tac gtg ggt cgc aag ccc				1508
Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro				
	375	380	385	
aag gtg gag cag ttg tcc aac atg att gtg cgc tcc tgc aag tgc agc				1556
Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser				
	390	395	400	
tga agccccgccc cgccccgccc ctcccggcag gcccgcccc gcccccgccc cgc				1612

<210> 17
 <211> 403
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<220>
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 <222> (1182)..(1196)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (1197)..(1220)
 <223> Encodes FLAG epitope tag

<220>
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 <222> (1182)..(1159)
 <223> Encodes ature fusion protein

<220>

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 <222> (1182)..(1159)
 <223> Encodes mature fusion protein

<400> 17

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
 85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
 115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
 130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
 145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
 210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
385 390 395 400

Lys Cys Ser

<210> 18
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
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ttcagctcca cgg 73

<210> 19
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
cttgctgctg tcataccttgt agtcgttatc cagggctcgg cggtggtgcc gggagctgtg 60
caggtgctgg gc 72

<210> 20
<211> 1624
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> CDS
<222> (348)..(1571)
<223>

<220>
<221> 5'UTR
<222> (1)..(347)
<223>

<220>
<221> 3'UTR
<222> (1572)..(1624)
<223>

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<223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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<222> (1197)..(1232)
<223> Encodes HA epitope tag

<220>
<221> misc_feature
<222> (1182)..(1571)
<223> Encodes mature fusion protein

<400> 20

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ctccctcgga cctgctggca gtagctcccc tatttaagaa caccactttt tggatctcag	120
agagcgctca tctcgatttt taccctgggtg gtatactgag acaccttggt gtcagagcct	180
caccgcgact cctgctgctt tctccctcaa cctcaaatta ttcaggacta tcacctacct	240
ttccttgga gacccacccc cacaagccct gcaggggcg ggcctccgca tcccaccttt	300
gccgagggtt cccgctctcc gaagtgcctt ggggcgcgcg ctcccc atg ccg ccc	356
	Met Pro Pro
	1
tcg ggg ctg cgg cta ctg ccg ctt ctg ctc cca ctc ccg tgg ctt cta	404
Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro Trp Leu Leu	
5 10 15	
gtg ctg acg ccc ggg agg cca gcc gcg gga ctc tcc acc tgc aag acc	452
Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr	
20 25 30 35	
atc gac atg gag ctg gtg aaa cgg aag cgc atc gaa gcc atc cgt ggc	500
Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly	
40 45 50	
cag atc ctg tcc aaa cta agg ctc gcc agt ccc cca agc cag ggg gag	548
Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu	
55 60 65	
gta ccg ccc ggc ccg ctg ccc gag gcg gtg ctc gct ttg tac aac agc	596
Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser	
70 75 80	
acc cgc gac cgg gtg gca ggc gag agc gcc gac cca gag ccg gag ccc	644
Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro	
85 90 95	
gaa gcg gac tac tat gct aaa gag gtc acc cgc gtg cta atg gtg gac	692
Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp	
100 105 110 115	
cgc aac aac gcc atc tat gag aaa acc aaa gac atc tca cac agt ata	740
Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile	
120 125 130	
tat atg ttc ttc aat acg tca gac att cgg gaa gca gtg ccc gaa ccc	788
Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro	
135 140 145	
cca ttg ctg tcc cgt gca gag ctg cgc ttg cag aga tta aaa tca agt	836
Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser	
150 155 160	
gtg gag caa cat gtg gaa ctc tac cag aaa tat agc aac aat tcc tgg	884
Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp	
165 170 175	
cgt tac ctt ggt aac cgg ctg ctg acc ccc act gat acg cct gag tgg	932
Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp	
180 185 190 195	

ctg tct ttt gac gtc act gga gtt gta cgg cag tgg ctg aac caa gga	980
Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu Asn Gln Gly	
200 205 210	
gac gga ata cag ggc ttt cga ttc agc gct cac tgc tct tgt gac agc	1028
Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser	
215 220 225	
aaa gat aac aaa ctc cac gtg gaa atc aac ggg atc agc ccc aaa cgt	1076
Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg	
230 235 240	
cgg ggc gac ctg ggc acc atc cat gac atg aac cgg ccc ttc ctg ctc	1124
Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu	
245 250 255	
ctc atg gcc acc ccc ctg gaa agg gcc cag cac ctg cac agc tca cgg	1172
Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg	
260 265 270 275	
cac cgg aga gcc ctg gat acc aac agc tac cca tac gac gtg cca gac	1220
His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp Val Pro Asp	
280 285 290	
tac gca tct ctg gcc ctg gat acc aac tat tgc ttc agc tcc aca gag	1268
Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu	
295 300 305	
aag aac tgc tgt gtg cgg cag ctg tac att gac ttt agg aag gac ctg	1316
Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu	
310 315 320	
ggt tgg aag tgg atc cac gag ccc aag ggc tac cat gcc aac ttc tgt	1364
Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys	
325 330 335	
ctg gga ccc tgc ccc tat att tgg agc ctg gac aca cag tac agc aag	1412
Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys	
340 345 350 355	
gtc ctt gcc ctc tac aac caa cac aac ccg ggc gct tcg gcg tca ccg	1460
Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro	
360 365 370	
tgc tgc gtg ccg cag gct ttg gag cca ctg ccc atc gtc tac tac gtg	1508
Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val	
375 380 385	
ggt cgc aag ccc aag gtg gag cag ttg tcc aac atg att gtg cgc tcc	1556
Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser	
390 395 400	
tgc aag tgc agc tga agccccgccc cgccccgccc ctcccggcag gcccgcccc	1611
Cys Lys Cys Ser	
405	
gcccccgccc cgc	1624

<210> 21

<211> 407
 <212> PRT
 <213> Artificial Sequence

<220>
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<220>
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 <222> (1182)..(1196)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
 <221> misc_feature
 <222> (1197)..(1232)
 <223> Encodes HA epitope tag

<220>
 <221> misc_feature
 <222> (1182)..(1571)
 <223> Encodes mature fusion protein

<400> 21

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu
 85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
 115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
 130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu

145

150

155

160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
 210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
 225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
 275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
 290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
 305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
 325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
 340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
 355 360 365

Ala Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
 370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
 385 390 395 400

Val Arg Ser Cys Lys Cys Ser
405

<210> 22
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
gccctggata ccaacagcta cccatacgac gtgccagact acgcatctct ggccctggat 60
accaactact gcttcagctc cacggagaag aactgctgcg tgcggcag 108

<210> 23
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
cagagatgcg tagtctggca cgtcgtatgg gtagctgttg gtatccaggg ctcggcggtg 60
ccgggagctg tgc 73

<210> 24
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion oligonucleotide

<220>
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<222> (1)..(1284)
<223>

<220>
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<222> (907)..(921)
<223> Encodes amino acid residues 1-5 of TGF-beta2

<220>
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<222> (922)..(945)
<223> Encodes FLAG epitope tag

<220>

<221> misc_feature
 <222> (907)..(1284)
 <223> Encodes mature fusion protein

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atg cac tac tgt gtg ctg agc acc ttt ttg ctc ctg cat ctg gtc ccg      48
Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
1                               5                               10                               15

gtg gcg ctc agt ctg tct acc tgc agc acc ctc gac atg gat cag ttt      96
Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
                20                               25                               30

atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc aag ctg      144
Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
                35                               40                               45

aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag gtc ccc      192
Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
                50                               55                               60

ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg cag gag      240
Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
        65                               70                               75                               80

aag gca agc cgg agg gca gcc gcc tgc gag cgc gag cgg agc gag cag      288
Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
                85                               90                               95

gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc cac ctc      336
Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
                100                               105                               110

ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac ttc aga      384
Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
                115                               120                               125

atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tgc aat ctg      432
Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
        130                               135                               140

gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa gcc aga      480
Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
        145                               150                               155                               160

gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc aaa gac      528
Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
                165                               170                               175

tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg aaa acc      576
Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
                180                               185                               190

aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct gtg cag      624
Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
                195                               200                               205

gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata agt tta      672
Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
        210                               215                               220

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cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc atc ccg	720
His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro	
225 230 235 240	
aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat ggc acc	768
Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr	
245 250 255	
tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act agg aaa	816
Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys	
260 265 270	
aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg ccc tcc	864
Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser	
275 280 285	
tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc gct ttg	912
Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu	
290 295 300	
gat gct gcc gac tac aag gat gac gac gac aag gct ttg gat gct gcc	960
Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala	
305 310 315 320	
tac tgc ttt aga aat gtg cag gat aat tgc tgc ctt cgc cct ctt tac	1008
Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr	
325 330 335	
att gat ttt aag agg gat ctt gga tgg aaa tgg atc cat gaa ccc aaa	1056
Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys	
340 345 350	
ggg tac aat gct aac ttc tgt gct ggg gca tgc cca tat cta tgg agt	1104
Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser	
355 360 365	
tca gac act caa cac acc aaa gtc ctc agc ctg tac aac acc ata aat	1152
Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn	
370 375 380	
ccc gaa gct tcc gct tcc cct tgc tgt gtg tcc cag gat ctg gaa cca	1200
Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro	
385 390 395 400	
ctg acc att ctc tat tac att gga aat acg ccc aag atc gaa cag ctt	1248
Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu	
405 410 415	
tcc aat atg att gtc aag tct tgt aaa tgc agc taa	1284
Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser	
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Met His Tyr Cys Val Leu Ser Thr Phe Leu Leu Leu His Leu Val Pro
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Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
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Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
          35          40          45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
          50          55          60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65          70          75          80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
          85          90          95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
          100          105          110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
          115          120          125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
          130          135          140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145          150          155          160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
          165          170          175

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Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
 180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
 195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
 210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
 225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
 245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
 260 265 270

Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
 275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
 290 295 300

Asp Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Ala Ala
 305 310 315 320

Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr
 325 330 335

Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys
 340 345 350

Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser
 355 360 365

Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr Asn Thr Ile Asn
 370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro
 385 390 395 400

Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys Ile Glu Gln Leu
 405 410 415

Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser
420 425

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<222> (929)..(964)
<223> Encodes HA epitope tag

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<222> (914)..(1303)
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Val Pro Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp
15 20 25 30

cag ttt atg cgc aag agg atc gag gcc atc cgc ggg cag atc ctg agc 145
Gln Phe Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser
35 40 45

aag ctg aag ctc acc agc ccc ccg gaa gac tat ccg gag ccg gat gag 193
Lys Leu Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu
50 55 60

gtc ccc ccg gag gtg att tcc atc tac aac agt acc agg gac tta ctg 241
Val Pro Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu

65	70	75	
cag gag aag gca agc cgg agg gca gcc gcc tgc gag cgc gag cgg agc Gln Glu Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser 80 85 90			289
gag cag gag tac tac gcc aag gag gtt tat aaa atc gac atg ccg tcc Glu Gln Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser 95 100 105 110			337
cac ctc ccc tcc gaa aat gcc atc ccg ccc act ttc tac aga ccc tac His Leu Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr 115 120 125			385
ttc aga atc gtc cgc ttt gat gtc tca aca atg gag aaa aat gct tcg Phe Arg Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser 130 135 140			433
aat ctg gtg aag gca gag ttc agg gtc ttc cgc ttg caa aac ccc aaa Asn Leu Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys 145 150 155			481
gcc aga gtg gcc gag cag cgg att gaa ctg tat cag atc ctt aaa tcc Ala Arg Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser 160 165 170			529
aaa gac tta aca tct ccc acc cag cgc tac atc gat agc aag gtt gtg Lys Asp Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val 175 180 185 190			577
aaa acc aga gcg gag ggt gaa tgg ctc tcc ttc gac gtg aca gac gct Lys Thr Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala 195 200 205			625
gtg cag gag tgg ctt cac cac aaa gac agg aac ctg ggg ttt aaa ata Val Gln Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile 210 215 220			673
agt tta cac tgc ccc tgc tgt acc ttc gtg ccg tct aat aat tac atc Ser Leu His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile 225 230 235			721
atc ccg aat aaa agc gaa gag ctc gag gcg aga ttt gca ggt att gat Ile Pro Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp 240 245 250			769
ggc acc tct aca tat gcc agt ggt gat cag aaa act ata aag tcc act Gly Thr Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr 255 260 265 270			817
agg aaa aaa acc agt ggg aag acc cca cat ctc ctg cta atg ttg ttg Arg Lys Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu 275 280 285			865
ccc tcc tac aga ctg gag tca caa cag tcc agc cgg cgg aag aag cgc Pro Ser Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg 290 295 300			913
gct ttg gat gct gcc agc tac cca tac gac gtg cca gac tac gca tct Ala Leu Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 305 310 315			961

ctg gct ttg gat gct gcc tac tgc ttt aga aat gtg cag gat aat tgc Leu Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys 320 325 330	1009
tgc ctt cgc cct ctt tac att gat ttt aag agg gat ctt gga tgg aaa Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys 335 340 345 350	1057
tgg atc cat gaa ccc aaa ggg tac aat gct aac ttc tgt gct ggg gca Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala 355 360 365	1105
tgc cca tat cta tgg agt tca gac act caa cac acc aaa gtc ctc agc Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser 370 375 380	1153
ctg tac aac acc ata aat ccc gaa gct tcc gct tcc cct tgc tgt gtg Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val 385 390 395	1201
tcc cag gat ctg gaa cca ctg acc att ctc tat tac att gga aat acg Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr 400 405 410	1249
ccc aag atc gaa cag ctt tcc aat atg att gtc aag tct tgt aaa tgc Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys 415 420 425 430	1297
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<220>
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 20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
 35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Asp Glu Val Pro
 50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
 65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Glu Gln
 85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Ser His Leu
 100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
 115 120 125

Ile Val Arg Phe Asp Val Ser Thr Met Glu Lys Asn Ala Ser Asn Leu
 130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
 145 150 155 160

Val Ala Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
 165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
 180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val Gln
 195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
 210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
 225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
 245 250 255

Ser Thr Tyr Ala Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

Lys Thr Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Ser Ser Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala
305 310 315 320

Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu
325 330 335

Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile
340 345 350

His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro
355 360 365

Tyr Leu Trp Ser Ser Asp Thr Gln His Thr Lys Val Leu Ser Leu Tyr
370 375 380

Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln
385 390 395 400

Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Asn Thr Pro Lys
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 aca atc agc ctc tct ctg tcc act tgc acc acg ttg gac ttc ggc cac 96
 Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
 20 25 30
 atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag 144
 Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
 35 40 45
 ctc agg ctc acc agc ccc cct gag cca tcg gtg atg acc cac gtc ccc 192
 Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
 50 55 60
 tat cag gtc ctg gca ctt tac aac agc acc cgg gag ttg ctg gaa gag 240
 Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
 65 70 75 80
 atg cac ggg gag agg gag gaa ggc tgc act cag gag acc tcg gag tct 288
 Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
 85 90 95
 gag tac tat gcc aaa gag atc cat aaa ttc gac atg atc cag gga ctg 336
 Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
 100 105 110
 gcg gag cac aat gaa ctg gcc gtc tgc ccc aaa gga att acc tct aag 384
 Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
 115 120 125
 gtt ttt cgt ttc aat gtg tcc tca gtg gag aaa aat gga acc aat ctg 432
 Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
 130 135 140
 ttc cgg gca gag ttc cgg gtc ttg cgg gtg ccc aac ccc agc tcc aag 480
 Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
 145 150 155 160
 cgc aca gag cag aga att gag ctc ttc cag ata ctt cga ccg gat gag 528
 Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
 165 170 175

cac ata gcc aag cag cgc tac ata ggt ggc aag aat ctg ccc aca agg	576
His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg	
180 185 190	
ggc acc gct gaa tgg ctg tct ttc gat gtc act gac act gtg cgc gag	624
Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu	
195 200 205	
tgg ctg ttg agg aga gag tcc aac ttg ggt ctg gaa atc agc atc cac	672
Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His	
210 215 220	
tgt cca tgt cac acc ttt cag ccc aat gga gac ata ctg gaa aat gtt	720
Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val	
225 230 235 240	
cat gag gtg atg gaa atc aaa ttc aaa gga gtg gac aat gaa gat gac	768
His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp	
245 250 255	
cat ggc cgt gga gac ctg ggg cgt ctc aag aag caa aag gat cac cac	816
His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His	
260 265 270	
aac cca cac ctg atc ctc atg atg atc ccc cca cac cga ctg gac agc	864
Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser	
275 280 285	
cca ggc cag ggc agt cag agg aag aag agg gcc ctg gac acc aat gac	912
Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp	
290 295 300	
tac aag gat gac gac gac aag gcc ctg gac acc aat tac tgc ttc cgc	960
Tyr Lys Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg	
305 310 315 320	
aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat att gac ttc cgg	1008
Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg	
325 330 335	
cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag ggt tac tat gcc	1056
Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala	
340 345 350	
aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc gca gac aca acc	1104
Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr	
355 360 365	
cat agc acg gtg ctt gga cta tac aac acc ctg aac cca gag gcg tct	1152
His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser	
370 375 380	
gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc ctg acc atc ttg	1200
Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu	
385 390 395 400	
tac tat gtg ggc aga acc ccc aag gtg gag cag ctg tcc aac atg gtg	1248
Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val	
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gtg aag tcg tgt aag tgc agc tga	1272

Val Lys Ser Cys Lys Cys Ser
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Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
 130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
 145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
 165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
 180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
 195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
 210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
 225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
 245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
 260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
 275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Asp
 290 295 300

Tyr Lys Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Arg
 305 310 315 320

Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg
 325 330 335

Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala
 340 345 350

Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr
 355 360 365

His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser

Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu
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Val Lys Ser Cys Lys Cys Ser
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<210> 30
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 Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
 20 25 30
 atc aag aag aag agg gtg gaa gcc att agg gga cag atc ttg agc aag 144
 Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
 35 40 45
 ctc agg ctc acc agc ccc cct gag cca tcg gtg atg acc cac gtc ccc 192

Leu	Arg	Leu	Thr	Ser	Pro	Pro	Glu	Pro	Ser	Val	Met	Thr	His	Val	Pro		
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Tyr	Gln	Val	Leu	Ala	Leu	Tyr	Asn	Ser	Thr	Arg	Glu	Leu	Leu	Glu	Glu		
65					70					75					80		
atg	cac	ggg	gag	agg	gag	gaa	ggc	tgc	act	cag	gag	acc	tcg	gag	tct	288	
Met	His	Gly	Glu	Arg	Glu	Glu	Gly	Cys	Thr	Gln	Glu	Thr	Ser	Glu	Ser		
				85					90						95		
gag	tac	tat	gcc	aaa	gag	atc	cat	aaa	ttc	gac	atg	atc	cag	gga	ctg	336	
Glu	Tyr	Tyr	Ala	Lys	Glu	Ile	His	Lys	Phe	Asp	Met	Ile	Gln	Gly	Leu		
			100					105						110			
gcg	gag	cac	aat	gaa	ctg	gcc	gtc	tgc	ccc	aaa	gga	att	acc	tct	aag	384	
Ala	Glu	His	Asn	Glu	Leu	Ala	Val	Cys	Pro	Lys	Gly	Ile	Thr	Ser	Lys		
		115					120						125				
gtt	ttt	cgt	ttc	aat	gtg	tcc	tca	gtg	gag	aaa	aat	gga	acc	aat	ctg	432	
Val	Phe	Arg	Phe	Asn	Val	Ser	Ser	Val	Glu	Lys	Asn	Gly	Thr	Asn	Leu		
	130					135						140					
ttc	cgg	gca	gag	ttc	cgg	gtc	ttg	cgg	gtg	ccc	aac	ccc	agc	tcc	aag	480	
Phe	Arg	Ala	Glu	Phe	Arg	Val	Leu	Arg	Val	Pro	Asn	Pro	Ser	Ser	Lys		
145					150					155					160		
cgc	aca	gag	cag	aga	att	gag	ctc	ttc	cag	ata	ctt	cga	ccg	gat	gag	528	
Arg	Thr	Glu	Gln	Arg	Ile	Glu	Leu	Phe	Gln	Ile	Leu	Arg	Pro	Asp	Glu		
				165					170						175		
cac	ata	gcc	aag	cag	cgc	tac	ata	ggt	ggc	aag	aat	ctg	ccc	aca	agg	576	
His	Ile	Ala	Lys	Gln	Arg	Tyr	Ile	Gly	Gly	Lys	Asn	Leu	Pro	Thr	Arg		
			180					185						190			
ggc	acc	gct	gaa	tgg	ctg	tct	ttc	gat	gtc	act	gac	act	gtg	cgc	gag	624	
Gly	Thr	Ala	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Asp	Thr	Val	Arg	Glu		
		195					200						205				
tgg	ctg	ttg	agg	aga	gag	tcc	aac	ttg	ggt	ctg	gaa	atc	agc	atc	cac	672	
Trp	Leu	Leu	Arg	Arg	Glu	Ser	Asn	Leu	Gly	Leu	Glu	Ile	Ser	Ile	His		
	210					215						220					
tgt	cca	tgt	cac	acc	ttt	cag	ccc	aat	gga	gac	ata	ctg	gaa	aat	gtt	720	
Cys	Pro	Cys	His	Thr	Phe	Gln	Pro	Asn	Gly	Asp	Ile	Leu	Glu	Asn	Val		
225					230					235					240		
cat	gag	gtg	atg	gaa	atc	aaa	ttc	aaa	gga	gtg	gac	aat	gaa	gat	gac	768	
His	Glu	Val	Met	Glu	Ile	Lys	Phe	Lys	Gly	Val	Asp	Asn	Glu	Asp	Asp		
				245					250						255		
cat	ggc	cgt	gga	gac	ctg	ggg	cgt	ctc	aag	aag	caa	aag	gat	cac	cac	816	
His	Gly	Arg	Gly	Asp	Leu	Gly	Arg	Leu	Lys	Lys	Gln	Lys	Asp	His	His		
			260					265						270			
aac	cca	cac	ctg	atc	ctc	atg	atg	atc	ccc	cca	cac	cga	ctg	gac	agc	864	
Asn	Pro	His	Leu	Ile	Leu	Met	Met	Ile	Pro	Pro	His	Arg	Leu	Asp	Ser		
		275					280							285			
cca	ggc	cag	ggc	agt	cag	agg	aag	aag	agg	gcc	ctg	gac	acc	aat	agc	912	
Pro	Gly	Gln	Gly	Ser	Gln	Arg	Lys	Lys	Arg	Ala	Leu	Asp	Thr	Asn	Ser		

290	295	300	
tac cca tac gac gtg cca gac tac gca tct ctg gcc ctg gac acc aat			960
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn			
305	310	315	320
tac tgc ttc cgc aac ctg gag gag aac tgc tgt gta cgc ccc ctt tat			1008
Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr			
	325	330	335
att gac ttc cgg cag gat cta ggc tgg aaa tgg gtc cac gaa cct aag			1056
Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys			
	340	345	350
ggt tac tat gcc aac ttc tgc tca ggc cct tgc cca tac ctc cgc agc			1104
Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser			
	355	360	365
gca gac aca acc cat agc acg gtg ctt gga cta tac aac acc ctg aac			1152
Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn			
	370	375	380
cca gag gcg tct gcc tcg cca tgc tgc gtc ccc cag gac ctg gag ccc			1200
Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro			
	385	390	400
ctg acc atc ttg tac tat gtg ggc aga acc ccc aag gtg gag cag ctg			1248
Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu			
	405	410	415
tcc aac atg gtg gtg aag tcg tgt aag tgc agc tga			1284
Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser			
	420	425	

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 <223> Encodes amino acid residues 1-5 of TGF-beta3

<220>
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 <222> (910)..(945)
 <223> Encodes HA epitope tag

<220>
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 <222> (895)..(1284)
 <223> Encodes mature fusion protein

<400> 31

Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn Leu Ala

1

5

10

15

Thr Ile Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe Gly His
20 25 30

Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys
35 40 45

Leu Arg Leu Thr Ser Pro Pro Glu Pro Ser Val Met Thr His Val Pro
50 55 60

Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu Glu Glu
65 70 75 80

Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Thr Ser Glu Ser
85 90 95

Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln Gly Leu
100 105 110

Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr Ser Lys
115 120 125

Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Gly Thr Asn Leu
130 135 140

Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser Ser Lys
145 150 155 160

Arg Thr Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro Asp Glu
165 170 175

His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro Thr Arg
180 185 190

Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val Arg Glu
195 200 205

Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser Ile His
210 215 220

Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu Asn Val
225 230 235 240

His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu Asp Asp
245 250 255

His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp His His
 260 265 270

Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu Asp Ser
 275 280 285

Pro Gly Gln Gly Ser Gln Arg Lys Lys Arg Ala Leu Asp Thr Asn Ser
 290 295 300

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn
 305 310 315 320

Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu Tyr
 325 330 335

Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys
 340 345 350

Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg Ser
 355 360 365

Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu Asn
 370 375 380

Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu Pro
 385 390 395 400

Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln Leu
 405 410 415

Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
 420 425

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 <213> Artificial Sequence

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 <222> (845)..(859)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (860)..(883)
 <223> Encodes FLAG epitope tag

<220>
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 <222> (845)..(1222)
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 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu
 1 5 10

ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga 97
 Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
 15 20 25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc 145
 Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
 30 35 40 45

atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc 193
 Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
 50 55 60

ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta 241
 Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
 65 70 75

ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc 289
 Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
 80 85 90

gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc 337
 Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr
 95 100 105

cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag 385
 Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys
 110 115 120 125

ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg	433
Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg	
130 135 140	
gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg	481
Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu	
145 150 155	
ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa	529
Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys	
160 165 170	
tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc	577
Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro	
175 180 185	
agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg	625
Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg	
190 195 200 205	
cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc	673
Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala	
210 215 220	
cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac	721
His Ser Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn	
225 230 235	
ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg	769
Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met	
240 245 250	
aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag	817
Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln	
255 260 265	
cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac gac tac	865
His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr	
270 275 280 285	
aag gat gac gac gac aag gcc ctg gat acc aac tac tgc ttc agc tcc	913
Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser	
290 295 300	
acg gag aag aac tgc tgc gtg cgg cag ctc tac att gac ttc cgg aag	961
Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys	
305 310 315	
gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc tac cat gcc aat	1009
Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn	
320 325 330	
ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta gac act cag tac	1057
Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr	
335 340 345	
agc aag gtc ctg gct ctg tac aac cag cac aac ccg ggc gcg tcg gcg	1105
Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala	
350 355 360 365	

gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg ccc atc gtg tac 1153
 Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr
 370 375 380

tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc gtg 1201
 Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val
 385 390 395

cgt tcc tgc aag tgc agc tga ggccccgccc cgcccacagc cccgcccacc 1252
 Arg Ser Cys Lys Cys Ser
 400

cggcaggccc ggccccaccc ccgcccgcct caccggggct gtattttaagg acatcgtgcc 1312

ccaagcccac ttgggatcga ttaaagcggc cgcgact 1349

<210> 33
 <211> 403
 <212> PRT
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<220>
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<220>
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 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <223> Encodes FLAG epitope tag

<220>
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 <222> (845)..(1222)
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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
 1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
 210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
 225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
 275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
 355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 385 390 395 400

Lys Cys Ser

<210> 34
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 <212> DNA
 <213> Artificial Sequence

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 <222> (1)..(14)
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 <222> (1227)..(1353)
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 <222> (849)..(863)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (864)..(887)
 <223> Encodes FLAG epitope tage

<220>
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 <222> (864)..(887)
 <223> Encodes FLAG epitope tag

<220>
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 <222> (849)..(1226)
 <223> Encodes mature fusion protein

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 1 5 10

ctg ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc 98
 Leu Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala
 15 20 25

gga ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag 146
 Gly Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys
 30 35 40

cgc atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc 194
 Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala
 45 50 55 60

agc ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca 242
 Ser Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala
 65 70 75

gta ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt 290
 Val Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser
 80 85 90

gtc gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc 338
 Val Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val
 95 100 105

acc cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc 386
 Thr Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe
 110 115 120

aag ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc 434
 Lys Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu
 125 130 135 140

cgg gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc 482
 Arg Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg
 145 150 155

ctg ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag 530
 Leu Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln
 160 165 170

aaa tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc 578
 Lys Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala
 175 180 185

ccc agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg Pro Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val 190 195 200	626
cgg cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt Arg Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser 205 210 215 220	674
gcc cac tgt tcc tgt gac agc aaa gat aac aca ctc cac gtg gaa att Ala His Cys Ser Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile 225 230 235	722
aac ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc Asn Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly 240 245 250	770
atg aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc Met Asn Arg Pro Phe Leu Leu Met Ala Thr Pro Leu Glu Arg Ala 255 260 265	818
cag cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac gac Gln His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp 270 275 280	866
tac aag gat gac gac gac aag gcc ctg gat acc aac tac tgc ttc agc Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser 285 290 295 300	914
tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att gac ttc cgg Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg 305 310 315	962
aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc tac cat gcc Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala 320 325 330	1010
aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta gac act cag Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln 335 340 345	1058
tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg ggc gcg tcg Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser 350 355 360	1106
gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg ccc atc gtg Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val 365 370 375 380	1154
tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile 385 390 395	1202
gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc cccgcccacc Val Arg Ser Cys Lys Cys Ser 400	1256
cggcaggccc ggccccaccc ccgcccgcct caccggggct gtatttaagg acatcgtgcc	1316
ccaagcccac ttgggatcga ttaaagcggc cgcgact	1353

<210> 35
 <211> 403
 <212> PRT
 <213> Artificial Sequence

<220>
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<220>
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 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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<220>
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 <222> (864)..(887)
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<220>
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 <222> (849)..(1226)
 <223> Encodes mature fusion protein

<400> 35

Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
 85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
 115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Asp Tyr Lys Asp Asp
275 280 285

Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
290 295 300

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
305 310 315 320

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
325 330 335

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
340 345 350

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
355 360 365

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 370 375 380

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 385 390 395 400

Lys Cys Ser

<210> 36
 <211> 1361
 <212> DNA
 <213> Artificial Sequence

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 <222> (845)..(859)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

<220>
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 <222> (860)..(895)
 <223> Encodes HA epitope tag

<220>
 <221> misc_feature
 <222> (845)..(1234)
 <223> Encodes mature fusion protein

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 1 5 10

49

ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly 15 20 25	97
ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg 30 35 40 45	145
atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser 50 55 60	193
ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val 65 70 75	241
ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val 80 85 90	289
gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc Glu Pro Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr 95 100 105	337
cgc gtg cta atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys 110 115 120 125	385
ggc acc ccc cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg 130 135 140	433
gaa gcg gtg ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg Glu Ala Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu 145 150 155	481
ctg agg ctc aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys 160 165 170	529
tac agc aat gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc Tyr Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro 175 180 185	577
agt gac tca ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg 190 195 200 205	625
cag tgg ctg acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala 210 215 220	673
cac tct tcc tct gac agc aaa gat aac aca ctc cac gtg gaa att aac His Ser Ser Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn 225 230 235	721
ggg ttc aat tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met 240 245 250	769

aac cgg ccc ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag	817
Asn Arg Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln	
255 260 265	
cac ctg cac agc tcc cgg cac cgc cga gcc ctg gat acc aac agc tac	865
His Leu His Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr	
270 275 280 285	
cca tac gac gtg cca gac tac gca tct ctg gcc ctg gat acc aac tac	913
Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr	
290 295 300	
tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg cag ctc tac att	961
Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile	
305 310 315	
gac ttc cgg aag gac ctg ggc tgg aag tgg att cat gaa ccc aag ggc	1009
Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly	
320 325 330	
tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac atc tgg agc cta	1057
Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu	
335 340 345	
gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg	1105
Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro	
350 355 360 365	
ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg	1153
Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu	
370 375 380	
ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc	1201
Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser	
385 390 395	
aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc	1254
Asn Met Ile Val Arg Ser Cys Lys Cys Ser	
400 405	
ccccccccacc cggcaggccc ggccccaccc ccgcccgcct caccgggggt gtattttaagg	1314
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 <222> (845)..(859)
 <223> Encodes amino acid residues 1-5 of TGF-beta1

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<223> Encodes HA epitope tag

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Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
210 215 220

Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
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Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
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ccg ctg ctg tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga 97
 Pro Leu Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly
 15 20 25

ctg tcc acc tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc 145
 Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg
 30 35 40 45

atc gag gcc att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc 193
 Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser
 50 55 60

ccc ccg agc cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta 241
 Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val
 65 70 75

ctg gct ctt tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc 289
 Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val
 80 85 90

gaa ccg gag ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc 337

Glu	Pro	Glu	Pro	Glu	Pro	Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr		
95						100					105						
cgc	gtg	cta	atg	gtg	gaa	agc	ggc	aac	caa	atc	tat	gat	aaa	ttc	aag	385	
Arg	Val	Leu	Met	Val	Glu	Ser	Gly	Asn	Gln	Ile	Tyr	Asp	Lys	Phe	Lys		
110					115					120					125		
ggc	acc	ccc	cac	agc	tta	tat	atg	ctg	ttc	aac	acg	tcg	gag	ctc	cgg	433	
Gly	Thr	Pro	His	Ser	Leu	Tyr	Met	Leu	Phe	Asn	Thr	Ser	Glu	Leu	Arg		
				130						135					140		
gaa	gcg	gtg	ccg	gaa	cct	gta	ttg	ctc	tct	cgg	gca	gag	ctg	cgc	ctg	481	
Glu	Ala	Val	Pro	Glu	Pro	Val	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu		
			145							150					155		
ctg	agg	ctc	aag	tta	aaa	gtg	gag	cag	cac	gtg	gag	cta	tac	cag	aaa	529	
Leu	Arg	Leu	Lys	Leu	Lys	Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys		
		160						165						170			
tac	agc	aat	gat	tcc	tgg	cgc	tac	ctc	agc	aac	cgg	ctg	ctg	gcc	ccc	577	
Tyr	Ser	Asn	Asp	Ser	Trp	Arg	Tyr	Leu	Ser	Asn	Arg	Leu	Leu	Ala	Pro		
		175				180						185					
agt	gac	tca	ccg	gag	tgg	ctg	tcc	ttt	gat	gtc	acc	gga	gtt	gtg	cgg	625	
Ser	Asp	Ser	Pro	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg		
190					195					200					205		
cag	tgg	ctg	acc	cgc	aga	gag	gct	ata	gag	ggc	ttt	cgc	ctc	agt	gcc	673	
Gln	Trp	Leu	Thr	Arg	Arg	Glu	Ala	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala		
				210					215						220		
cac	tgt	tcc	tgt	gac	agc	aaa	gat	aac	aca	ctc	cac	gtg	gaa	att	aac	721	
His	Cys	Ser	Cys	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn		
			225					230						235			
ggg	ttc	aat	tct	ggc	cgc	cgg	ggt	gac	ctg	gcc	acc	att	cac	ggc	atg	769	
Gly	Phe	Asn	Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met		
		240					245					250					
aac	cgg	ccc	ttc	ctg	ctc	ctc	atg	gcc	acc	ccg	ctg	gag	agg	gcc	cag	817	
Asn	Arg	Pro	Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln		
		255					260							265			
cac	ctg	cac	agc	tcc	cgg	cac	cgc	cga	gcc	ctg	gat	acc	aac	agc	tac	865	
His	Leu	His	Ser	Ser	Arg	His	Arg	Arg	Ala	Leu	Asp	Thr	Asn	Ser	Tyr		
					275						280				285		
cca	tac	gac	gtg	cca	gac	tac	gca	tct	ctg	gcc	ctg	gat	acc	aac	tac	913	
Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser	Leu	Ala	Leu	Asp	Thr	Asn	Tyr		
				290						295					300		
tgc	ttc	agc	tcc	acg	gag	aag	aac	tgc	tgc	gtg	cgg	cag	ctc	tac	att	961	
Cys	Phe	Ser	Ser	Thr	Glu	Lys	Asn	Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile		
				305				310							315		
gac	ttc	cgg	aag	gac	ctg	ggc	tgg	aag	tgg	att	cat	gaa	ccc	aag	ggc	1009	
Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp	Lys	Trp	Ile	His	Glu	Pro	Lys	Gly		
			320				325							330			
tac	cat	gcc	aat	ttc	tgc	ctg	ggg	ccc	tgt	ccc	tac	atc	tgg	agc	cta	1057	
Tyr	His	Ala	Asn	Phe	Cys	Leu	Gly	Pro	Cys	Pro	Tyr	Ile	Trp	Ser	Leu		

335

340

345

gac act cag tac agc aag gtc ctg gct ctg tac aac cag cac aac ccg 1105
 Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro
 350 355 360 365

ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag cca ctg 1153
 Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu
 370 375 380

ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc 1201
 Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser
 385 390 395

aac atg atc gtg cgt tcc tgc aag tgc agc tga ggccccgccc cgccccacagc 1254
 Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 400 405

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Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
 35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
225 230 235 240

Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Ser Tyr Pro Tyr Asp
275 280 285

Val Pro Asp Tyr Ala Ser Leu Ala Leu Asp Thr Asn Tyr Cys Phe Ser
290 295 300

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg
305 310 315 320

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala
325 330 335

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln
340 345 350

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser
355 360 365

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val
370 375 380

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile
385 390 395 400

Val Arg Ser Cys Lys Cys Ser
405